

SEQUENCE LISTING

<110> Kennedy, Giulia
Kang, Sanmao
Reinhard, Christoph
Jefferson, Anne Bennett

<120> POLYNUCLEOTIDES RELATED TO COLON CANCER

<130> 2300-1663

<140> Unassigned

<141> 2001-06-14

<150> 60/211,835

<151> 2000-06-15

<160> 127

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<211> 564

<212> DNA

<213> H. sapiens

<220>

<221> CDS

<222> (21)...(396)

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53

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1				5					10	

cat gtg cgg ggg gtg ggg tcc cgt ggc ttc ccc ctg cgc ctc cag gcc
101

His	Val	Arg	Gly	Val	Gly	Ser	Arg	Gly	Phe	Pro	Leu	Arg	Leu	Gln	Ala
			15					20						25	

acc gag gtc cgt atc tgc cct gtg gaa ttc aac ccc aac ttc gtg gcg
149

Thr	Glu	Val	Arg	Ile	Cys	Pro	Val	Glu	Phe	Asn	Pro	Asn	Phe	Val	Ala
		30					35					40			

cgt atg ata cct aaa gtg gag tgg tcg gcg ttc ctg gag gcg gcc gat
197

Arg	Met	Ile	Pro	Lys	Val	Glu	Trp	Ser	Ala	Phe	Leu	Glu	Ala	Ala	Asp
	45					50					55				

aac ttg cgt ctg atc cag gtg ccg aaa ggg ccg gtt gag gga tat gag
245

Asn	Leu	Arg	Leu	Ile	Gln	Val	Pro	Lys	Gly	Pro	Val	Glu	Gly	Tyr	Glu
	60				65					70					75

gag aat gag gag ttt ctg agg acc atg cac cac ctg ctg ctg gag gtg
293

Glu Asn Glu Glu Phe Leu Arg Thr Met His His Leu Leu Leu Glu Val
80 85 90

gaa gtg ata gag ggc acc ctg cag tgc ccg gaa tct gga cgt atg ttc
341

Glu Val Ile Glu Gly Thr Leu Gln Cys Pro Glu Ser Gly Arg Met Phe
95 100 105

ccc atc agc cgc ggg atc ccc aac atg ctg ctg agt gaa gag gaa act
389

Pro Ile Ser Arg Gly Ile Pro Asn Met Leu Leu Ser Glu Glu Glu Thr
110 115 120

gag agt t gattgtgcca ggcgccagtt tttcttgta tgactgtgta tttttgtga
446

Glu Ser
125

tctataccct gtttcgaat tctgccgtgt gtatcccaa cccttgaccc aatgacacca
506

aacacagtgt ttttgagctc ggtattatat atttttttct cattaaaggt ttaaaacc
564

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<213> H. sapiens

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Gly Ser Arg Gly Phe Pro Leu Arg Leu Gln Ala Thr Glu Val Arg Ile
20 25 30

Cys Pro Val Glu Phe Asn Pro Asn Phe Val Ala Arg Met Ile Pro Lys
35 40 45

Val Glu Trp Ser Ala Phe Leu Glu Ala Ala Asp Asn Leu Arg Leu Ile
50 55 60

Gln Val Pro Lys Gly Pro Val Glu Gly Tyr Glu Glu Asn Glu Glu Phe
65 70 75 80

Leu Arg Thr Met His His Leu Leu Leu Glu Val Glu Val Ile Glu Gly
85 90 95

Thr Leu Gln Cys Pro Glu Ser Gly Arg Met Phe Pro Ile Ser Arg Gly
100 105 110

Ile Pro Asn Met Leu Leu Ser Glu Glu Glu Thr Glu Ser
115 120 125

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<222> (219) ... (693)

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agctggggcg cggtgccaa gggccggccc ggaagtccca gcggtcttta aattctcccg
120

tgctagggcc agcctgcgca ttcttacctg tcgggggtgcg gcgagtgtct cacctctctg
180

cacttccaag gactcttgct atctgcctta ggcgggaa atg ctg ttg ctg gat tgc
236

Met Leu Leu Leu Asp Cys
1 5

aac ccc gag gtg gat ggt ctg aag cat ttg ctg gag aca ggg gcc tcg
284

Asn Pro Glu Val Asp Gly Leu Lys His Leu Leu Glu Thr Gly Ala Ser
10 15 20

gtc aac gca ccc ccg gat ccc tgc aag cag tcg cct gtc cac tta gcc
332

Val Asn Ala Pro Pro Asp Pro Cys Lys Gln Ser Pro Val His Leu Ala
25 30 35

gca gga agc ggc ctt gct tgc ttt ctt ctc tgg cag ctg caa acg ggc
380

Ala Gly Ser Gly Leu Ala Cys Phe Leu Leu Trp Gln Leu Gln Thr Gly
40 45 50

gct gac ctc aac cag cag gat gtt tta gga gaa gct cca cta cac aag
428

Ala Asp Leu Asn Gln Gln Asp Val Leu Gly Glu Ala Pro Leu His Lys
55 60 65 70

gca gca aaa gtt gga agc ctg gag tgc cta agc ctg ctt gta gcc agt
476

Ala Ala Lys Val Gly Ser Leu Glu Cys Leu Ser Leu Leu Val Ala Ser
75 80 85

gat gcc caa att gat tta tgt aat aag aac ggg caa aca gct gaa gat
524

Asp Ala Gln Ile Asp Leu Cys Asn Lys Asn Gly Gln Thr Ala Glu Asp
90 95 100

ctc gct tgg tca tgt gga ttt cca gac tgt gcc aag ttt ctt aca aca
572

Leu Ala Trp Ser Cys Gly Phe Pro Asp Cys Ala Lys Phe Leu Thr Thr
105 110 115

att aaa tgt atg cag aca ata aaa gca agt gaa cac cct gac agg aat
620

Ile Lys Cys Met Gln Thr Ile Lys Ala Ser Glu His Pro Asp Arg Asn
120 125 130

gat tgt gtt gcc gtg ctc aga cag aaa cgg agt ctc gga agt gta gaa
668

Asp Cys Val Ala Val Leu Arg Gln Lys Arg Ser Leu Gly Ser Val Glu
135 140 145 150

aat acc agt ggg aaa agg aag tgc t gatgtcacgt gggttatgaa

713

Asn Thr Ser Gly Lys Arg Lys Cys

155

gaagtctgaa gaacgccttc atttcatgca aatctataag ctctctgcttt tggctttacc

773

atatgttggtg tctaattctcc ttctgagaag gacgaaaaac tttcttccaa gtgaagatcc

833

atttaagaac acatgtatattt acatgcctat aatatgctgg ttgtgtatgc tttgtctttt

893

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919

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<211> 158

<212> PRT

<213> H. sapiens

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1

5

10

15

Leu Glu Thr Gly Ala Ser Val Asn Ala Pro Pro Asp Pro Cys Lys Gln

20

25

30

Ser Pro Val His Leu Ala Ala Gly Ser Gly Leu Ala Cys Phe Leu Leu

35

40

45

Trp Gln Leu Gln Thr Gly Ala Asp Leu Asn Gln Gln Asp Val Leu Gly

50

55

60

Glu Ala Pro Leu His Lys Ala Ala Lys Val Gly Ser Leu Glu Cys Leu

65

70

75

80

Ser Leu Leu Val Ala Ser Asp Ala Gln Ile Asp Leu Cys Asn Lys Asn

85

90

95

Gly Gln Thr Ala Glu Asp Leu Ala Trp Ser Cys Gly Phe Pro Asp Cys

100

105

110

Ala Lys Phe Leu Thr Thr Ile Lys Cys Met Gln Thr Ile Lys Ala Ser

115

120

125

Glu His Pro Asp Arg Asn Asp Cys Val Ala Val Leu Arg Gln Lys Arg

130

135

140

Ser Leu Gly Ser Val Glu Asn Thr Ser Gly Lys Arg Lys Cys

145

150

155

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<221> CDS

<222> (5)...(1760)

<400> 5

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49

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1

5

10

15

ctg tac atg gtg aat gga cca cca cat ttt aca gaa agc aca gtg ttt

97

Leu Tyr Met Val Asn Gly Pro Pro His Phe Thr Glu Ser Thr Val Phe
20 25 30

cca agg gaa tct ggg aag aat tgc aaa gtc tgt atc ttt agt aag gat
145
Pro Arg Glu Ser Gly Lys Asn Cys Lys Val Cys Ile Phe Ser Lys Asp
35 40 45

ggg acc ttg ttt gcc tgg ggc aat gga gaa aaa gta aat att atc agt
193
Gly Thr Leu Phe Ala Trp Gly Asn Gly Glu Lys Val Asn Ile Ile Ser
50 55 60

gtc act aac aag gga cta ctg cac tcc ttc gac ctc ctg aag gca gtt
241
Val Thr Asn Lys Gly Leu Leu His Ser Phe Asp Leu Leu Lys Ala Val
65 70 75

tgc ctt gaa ttc tca ccc aaa aat act gtc ctg gca acg tgg cag cct
289
Cys Leu Glu Phe Ser Pro Lys Asn Thr Val Leu Ala Thr Trp Gln Pro
80 85 90 95

tac act act tct aaa gat ggc aca gct ggg ata ccc aac cta caa ctt
337
Tyr Thr Thr Ser Lys Asp Gly Thr Ala Gly Ile Pro Asn Leu Gln Leu
100 105 110

tat gat gtg aaa act ggg aca tgt ttg aaa tct ttc atc cag aaa aaa
385
Tyr Asp Val Lys Thr Gly Thr Cys Leu Lys Ser Phe Ile Gln Lys Lys
115 120 125

atg caa aat tgg tgt cca tcc tgg tca gaa gat gaa act ctt tgt gcc
433
Met Gln Asn Trp Cys Pro Ser Trp Ser Glu Asp Glu Thr Leu Cys Ala
130 135 140

cgc aat gtt aac aat gaa gtt cac ttc ttt gaa aac aac aat ttt aac
481
Arg Asn Val Asn Asn Glu Val His Phe Phe Glu Asn Asn Asn Phe Asn
145 150 155

aca att gca aat aaa ttg cat ttg caa aaa att aat gac ttt gta tta
529
Thr Ile Ala Asn Lys Leu His Leu Gln Lys Ile Asn Asp Phe Val Leu
160 165 170 175

tca cct gga ccc caa cca tac aag gtg gct gtc tat gtt cca gga agt
577
Ser Pro Gly Pro Gln Pro Tyr Lys Val Ala Val Tyr Val Pro Gly Ser
180 185 190

aaa ggt gca cct tca ttt gtt aga tta tat cag tac ccc aac ttt gct
625
Lys Gly Ala Pro Ser Phe Val Arg Leu Tyr Gln Tyr Pro Asn Phe Ala
195 200 205

gga cct cat gca gct tta gct aat aaa agt ttc ttt aag gca gat aaa
673

Gly Pro His Ala Ala Leu Ala Asn Lys Ser Phe Phe Lys Ala Asp Lys
210 215 220

gtt aca atg ctg tgg aat aaa aaa gct act gct gtg ttg gta ata gct
721

Val Thr Met Leu Trp Asn Lys Lys Ala Thr Ala Val Leu Val Ile Ala
225 230 235

agc aca gat gtt gac aag aca gga gct tcc tac tat gga gaa caa act
769

Ser Thr Asp Val Asp Lys Thr Gly Ala Ser Tyr Tyr Gly Glu Gln Thr
240 245 250 255

cta cac tac att gca aca aat gga gaa agt gct gta gtg caa tta cca
817

Leu His Tyr Ile Ala Thr Asn Gly Glu Ser Ala Val Val Gln Leu Pro
260 265 270

aaa aat ggc ccc att tat gat gta gtt tgg aat tct agt tct act gag
865

Lys Asn Gly Pro Ile Tyr Asp Val Val Trp Asn Ser Ser Ser Thr Glu
275 280 285

ttt tgt gct gta tat ggt ttt atg cct gcc aaa gcg aca att ttc aac
913

Phe Cys Ala Val Tyr Gly Phe Met Pro Ala Lys Ala Thr Ile Phe Asn
290 295 300

ttg aaa tgt gat cct gta ttt gac ttt gga act ggt cct cgt aat gca
961

Leu Lys Cys Asp Pro Val Phe Asp Phe Gly Thr Gly Pro Arg Asn Ala
305 310 315

gcc tac tat agc cct cat gga cat ata tta gta tta gct gga ttt gga
1009

Ala Tyr Tyr Ser Pro His Gly His Ile Leu Val Leu Ala Gly Phe Gly
320 325 330 335

aat ctg agg gga caa atg gaa gtg tgg gat gtg aaa aac tac aaa ctt
1057

Asn Leu Arg Gly Gln Met Glu Val Trp Asp Val Lys Asn Tyr Lys Leu
340 345 350

att tct aaa ccg gtg gct tct gat tct aca tat ttt gct tgg tgc ccg
1105

Ile Ser Lys Pro Val Ala Ser Asp Ser Thr Tyr Phe Ala Trp Cys Pro
355 360 365

gat ggt gag cat att tta aca gct aca tgt gct ccc agg tta cgg gtt
1153

Asp Gly Glu His Ile Leu Thr Ala Thr Cys Ala Pro Arg Leu Arg Val
370 375 380

09883152 061504

aat aat gga tac aaa att tgg cat tat act ggc tct atc ttg cac aag
1201
Asn Asn Gly Tyr Lys Ile Trp His Tyr Thr Gly Ser Ile Leu His Lys
385 390 395

tat gat gtg cca tca aat gca gaa tta tgg cag gtt tct tgg cag cca
1249
Tyr Asp Val Pro Ser Asn Ala Glu Leu Trp Gln Val Ser Trp Gln Pro
400 405 410 415

ttt ttg gat gga ata ttt cca gca aaa aca ata act tac caa gca gtt
1297
Phe Leu Asp Gly Ile Phe Pro Ala Lys Thr Ile Thr Tyr Gln Ala Val
420 425 430

cca agt gaa gta ccc aat gag gaa cct aaa gtt gca aca gct tat aga
1345
Pro Ser Glu Val Pro Asn Glu Glu Pro Lys Val Ala Thr Ala Tyr Arg
435 440 445

ccc cca gct tta aga aat aaa cca atc acc aat tcc aaa ttg cat gaa
1393
Pro Pro Ala Leu Arg Asn Lys Pro Ile Thr Asn Ser Lys Leu His Glu
450 455 460

gag gaa cca cct cag aat atg aaa cca caa tca gga aac gat aag cca
1441
Glu Glu Pro Pro Gln Asn Met Lys Pro Gln Ser Gly Asn Asp Lys Pro
465 470 475

tta tca aaa aca gct ctt aaa aat caa agg aag cat gaa gct aag aaa
1489
Leu Ser Lys Thr Ala Leu Lys Asn Gln Arg Lys His Glu Ala Lys Lys
480 485 490 495

gct gca aag cag gaa gca aga agt gac aag agt cca gat ttg gca cct
1537
Ala Ala Lys Gln Glu Ala Arg Ser Asp Lys Ser Pro Asp Leu Ala Pro
500 505 510

act cct gcc cca cag agc aca cca cga aac act gtc tct cag tca att
1585
Thr Pro Ala Pro Gln Ser Thr Pro Arg Asn Thr Val Ser Gln Ser Ile
515 520 525

tct ggg gac cct gag ata gac aaa aaa atc aag aac cta aag aag aaa
1633
Ser Gly Asp Pro Glu Ile Asp Lys Lys Ile Lys Asn Leu Lys Lys Lys
530 535 540

ctg aaa gca atc gaa caa ctg aaa gaa caa gca gca act gga aaa cag
1681
Leu Lys Ala Ile Glu Gln Leu Lys Glu Gln Ala Ala Thr Gly Lys Gln
545 550 555

cta gaa aaa aat cag ttg gag aaa att cag aaa gaa aca gcc ctt ctc
1729

Leu Glu Lys Asn Gln Leu Glu Lys Ile Gln Lys Glu Thr Ala Leu Leu
 560 565 570 575

cag gag ctg gaa gat ttg gaa ttg ggt att t aaagattcac ggaaagcaag
 1780

Gln Glu Leu Glu Asp Leu Glu Leu Gly Ile
 580 585

ttgatgacca gaaatcagtg caaacacatc ttctgttaaa cccattggta tacacagaat
 1840
 attcctgtgc ccacacttaa tgtcaatcta taattttaac catttatcca agattctact
 1900
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 1949

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 <212> PRT
 <213> H. sapiens

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 Arg Glu Ser Gly Lys Asn Cys Lys Val Cys Ile Phe Ser Lys Asp Gly
 35 40 45
 Thr Leu Phe Ala Trp Gly Asn Gly Glu Lys Val Asn Ile Ile Ser Val
 50 55 60
 Thr Asn Lys Gly Leu Leu His Ser Phe Asp Leu Leu Lys Ala Val Cys
 65 70 75 80
 Leu Glu Phe Ser Pro Lys Asn Thr Val Leu Ala Thr Trp Gln Pro Tyr
 85 90 95
 Thr Thr Ser Lys Asp Gly Thr Ala Gly Ile Pro Asn Leu Gln Leu Tyr
 100 105 110
 Asp Val Lys Thr Gly Thr Cys Leu Lys Ser Phe Ile Gln Lys Lys Met
 115 120 125
 Gln Asn Trp Cys Pro Ser Trp Ser Glu Asp Glu Thr Leu Cys Ala Arg
 130 135 140
 Asn Val Asn Asn Glu Val His Phe Phe Glu Asn Asn Asn Phe Asn Thr
 145 150 155 160
 Ile Ala Asn Lys Leu His Leu Gln Lys Ile Asn Asp Phe Val Leu Ser
 165 170 175
 Pro Gly Pro Gln Pro Tyr Lys Val Ala Val Tyr Val Pro Gly Ser Lys
 180 185 190
 Gly Ala Pro Ser Phe Val Arg Leu Tyr Gln Tyr Pro Asn Phe Ala Gly
 195 200 205
 Pro His Ala Ala Leu Ala Asn Lys Ser Phe Phe Lys Ala Asp Lys Val
 210 215 220
 Thr Met Leu Trp Asn Lys Lys Ala Thr Ala Val Leu Val Ile Ala Ser
 225 230 235 240
 Thr Asp Val Asp Lys Thr Gly Ala Ser Tyr Tyr Gly Glu Gln Thr Leu
 245 250 255
 His Tyr Ile Ala Thr Asn Gly Glu Ser Ala Val Val Gln Leu Pro Lys
 260 265 270
 Asn Gly Pro Ile Tyr Asp Val Val Trp Asn Ser Ser Ser Thr Glu Phe
 275 280 285

09883152.061501

Cys Ala Val Tyr Gly Phe Met Pro Ala Lys Ala Thr Ile Phe Asn Leu
 290 295 300
 Lys Cys Asp Pro Val Phe Asp Phe Gly Thr Gly Pro Arg Asn Ala Ala
 305 310 315 320
 Tyr Tyr Ser Pro His Gly His Ile Leu Val Leu Ala Gly Phe Gly Asn
 325 330 335
 Leu Arg Gly Gln Met Glu Val Trp Asp Val Lys Asn Tyr Lys Leu Ile
 340 345 350
 Ser Lys Pro Val Ala Ser Asp Ser Thr Tyr Phe Ala Trp Cys Pro Asp
 355 360 365
 Gly Glu His Ile Leu Thr Ala Thr Cys Ala Pro Arg Leu Arg Val Asn
 370 375 380
 Asn Gly Tyr Lys Ile Trp His Tyr Thr Gly Ser Ile Leu His Lys Tyr
 385 390 395 400
 Asp Val Pro Ser Asn Ala Glu Leu Trp Gln Val Ser Trp Gln Pro Phe
 405 410 415
 Leu Asp Gly Ile Phe Pro Ala Lys Thr Ile Thr Tyr Gln Ala Val Pro
 420 425 430
 Ser Glu Val Pro Asn Glu Glu Pro Lys Val Ala Thr Ala Tyr Arg Pro
 435 440 445
 Pro Ala Leu Arg Asn Lys Pro Ile Thr Asn Ser Lys Leu His Glu Glu
 450 455 460
 Glu Pro Pro Gln Asn Met Lys Pro Gln Ser Gly Asn Asp Lys Pro Leu
 465 470 475 480
 Ser Lys Thr Ala Leu Lys Asn Gln Arg Lys His Glu Ala Lys Lys Ala
 485 490 495
 Ala Lys Gln Glu Ala Arg Ser Asp Lys Ser Pro Asp Leu Ala Pro Thr
 500 505 510
 Pro Ala Pro Gln Ser Thr Pro Arg Asn Thr Val Ser Gln Ser Ile Ser
 515 520 525
 Gly Asp Pro Glu Ile Asp Lys Lys Ile Lys Asn Leu Lys Lys Lys Leu
 530 535 540
 Lys Ala Ile Glu Gln Leu Lys Glu Gln Ala Ala Thr Gly Lys Gln Leu
 545 550 555 560
 Glu Lys Asn Gln Leu Glu Lys Ile Gln Lys Glu Thr Ala Leu Leu Gln
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 110
 Met Ala Asn Ser Gly Cys Lys Asp Val Thr Gly
 1 5 10

 cca gat gag gag agt ttt ctg tac ttt gcc tac ggc agc aac ctg ctg
 158

09883152-061501

Pro Asp Glu Glu Ser Phe Leu Tyr Phe Ala Tyr Gly Ser Asn Leu Leu
15 20 25

aca gag agg atc cac ctc cga aac ccc tcg gcg gcg ttc ttc tgt gtg
206

Thr Glu Arg Ile His Leu Arg Asn Pro Ser Ala Ala Phe Phe Cys Val
30 35 40

gcc cgc ctg cag gat ttt aag ctt gac ttt ggc aat tcc caa ggc aaa
254

Ala Arg Leu Gln Asp Phe Lys Leu Asp Phe Gly Asn Ser Gln Gly Lys
45 50 55

aca agt caa act tgg cat gga ggg ata gcc acc att ttt cag agt cct
302

Thr Ser Gln Thr Trp His Gly Gly Ile Ala Thr Ile Phe Gln Ser Pro
60 65 70 75

ggc gat gaa gtg tgg gga gta gta tgg aaa atg aac aaa agc aat tta
350

Gly Asp Glu Val Trp Gly Val Val Trp Lys Met Asn Lys Ser Asn Leu
80 85 90

aat tct ctg gat gag caa gaa ggg gtt aaa agt gga atg tat gtt gta
398

Asn Ser Leu Asp Glu Gln Glu Gly Val Lys Ser Gly Met Tyr Val Val
95 100 105

ata gaa gtt aaa gtt gca act caa gaa gga aaa gaa ata acc tgt cga
446

Ile Glu Val Lys Val Ala Thr Gln Glu Gly Lys Glu Ile Thr Cys Arg
110 115 120

agt tat ctg atg aca aat tac gaa agt gct ccc cca tcc cca cag tat
494

Ser Tyr Leu Met Thr Asn Tyr Glu Ser Ala Pro Pro Ser Pro Gln Tyr
125 130 135

aaa aag att att tgc atg ggt gca aaa gaa aat ggt ttg ccg ctg gag
542

Lys Lys Ile Ile Cys Met Gly Ala Lys Glu Asn Gly Leu Pro Leu Glu
140 145 150 155

tat caa gag aag tta aaa gca ata gaa cca aat gac tat aca gga aag
590

Tyr Gln Glu Lys Leu Lys Ala Ile Glu Pro Asn Asp Tyr Thr Gly Lys
160 165 170

gtc tca gaa gaa att gaa gac atc atc aaa aag ggg gaa aca caa act
638

Val Ser Glu Glu Ile Glu Asp Ile Ile Lys Lys Gly Glu Thr Gln Thr
175 180 185

ctt t agaacataac agaatatatc taagggtatt ctatgtgcta atataaaaata
692

Leu

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 752
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 812
 gataggagtt agacaattta aaaggggtgt atgagggcct gaaatatgtg acaaataaat
 872
 gtgagtaccc cttctgtgaa cactgaaagc tattctcttg aattgatctt aagtgtctcc
 932
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 992
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 1110

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 35 40 45
 Phe Lys Leu Asp Phe Gly Asn Ser Gln Gly Lys Thr Ser Gln Thr Trp
 50 55 60
 His Gly Gly Ile Ala Thr Ile Phe Gln Ser Pro Gly Asp Glu Val Trp
 65 70 75 80
 Gly Val Val Trp Lys Met Asn Lys Ser Asn Leu Asn Ser Leu Asp Glu
 85 90 95
 Gln Glu Gly Val Lys Ser Gly Met Tyr Val Val Ile Glu Val Lys Val
 100 105 110
 Ala Thr Gln Glu Gly Lys Glu Ile Thr Cys Arg Ser Tyr Leu Met Thr
 115 120 125
 Asn Tyr Glu Ser Ala Pro Pro Ser Pro Gln Tyr Lys Lys Ile Ile Cys
 130 135 140
 Met Gly Ala Lys Glu Asn Gly Leu Pro Leu Glu Tyr Gln Glu Lys Leu
 145 150 155 160
 Lys Ala Ile Glu Pro Asn Asp Tyr Thr Gly Lys Val Ser Glu Glu Ile
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 Glu Asp Ile Ile Lys Lys Gly Glu Thr Gln Thr Leu
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111

Met Ala Asn Ser Gly Cys Lys Asp Val Thr Gly
1 5 10

cca gat gag gag agt ttt ctg tac ttt gcc tac ggc agc aac ctg ctg
159

Pro Asp Glu Glu Ser Phe Leu Tyr Phe Ala Tyr Gly Ser Asn Leu Leu
15 20 25

aca gag agg atc cac ctc cga aac ccc tcg gcg gcg ttc ttc tgt gtg
207

Thr Glu Arg Ile His Leu Arg Asn Pro Ser Ala Ala Phe Phe Cys Val
30 35 40

gcc cgc ctg cag gca aga agg ggt t aaaagtggaa tgtatgttgt
252

Ala Arg Leu Gln Ala Arg Arg Gly
45 50

aatagaagtt aaagttgcaa ctcaagaagg aaaagaaata acctgtcgaa gttatctgat
312

gacaaattac gaaagtgctc ccccatcccc acagtataaa aagattattt gcatgggtgc
372

aaaagaaaaat ggtttgccgc tggagtatca agagaagtta aaagcaatag aaccaaata
432

ctatacagga aaggtctcag aagaaattga agacatcatc aaaaaggggg aaacacaaac
492

tctttagaac ataacagaat atatctaagg gtattctatg tgctaataata aaatattttt
552

aacacttgag aacagggatc tgggggatct ccacgtttga tccattttca gcagtgtctt
612

gaaggagtat cttacttggg tgattccttg tttttagact ataaaaagaa actgggatag
672

gagttagaca atttaaaagg ggtgtatgag ggcttgaaat atgtgacaaa tgaatgtgag
732

taccccttct gtgaacactg aaagctatct tcttgaattg atcttaagtg tctccttgct
792

ctggtaaaag atagatttgt agctcacttg atgatgggtgc tgggtgaattg ctctgctctg
852

tctgagattt ttaaaaaatca gcttaatgag agtaatctgc agacaattga taataacatt
912

ttgaaaattg gaaagatggg atactgtttt tagaggaata aacgtatttg tgg
965

<210> 10

<211> 51

<212> PRT

<213> H. sapiens

<400> 10

Met Ala Asn Ser Gly Cys Lys Asp Val Thr Gly Pro Asp Glu Glu Ser
1 5 10 15

Phe Leu Tyr Phe Ala Tyr Gly Ser Asn Leu Leu Thr Glu Arg Ile His
20 25 30

Leu Arg Asn Pro Ser Ala Ala Phe Phe Cys Val Ala Arg Leu Gln Ala
 35 40 45

Arg Arg Gly
 50

<210> 11

<211> 658

<212> DNA

<213> H. sapiens

<400> 11

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 cccctgcccc ggaccagccc ctggtggaag ccaaccacct gctgcacgag agcgacacgg
 120
 acaaggacgg gcggctgagc aaagcgaaa tctgggtaa ttggaacatg tttgtgggca
 180
 gtcaggccac caactatggt gaggacctga cccggcacca cgatgagctg tgagccccgc
 240
 gcacctgcca cagcctcaga ggcccgaca atgaccggag gaggggccgc tgtggtctgg
 300
 cccctccct gtccaggccc cgcaggaggc agatgcagtc ccaggcatcc tctgcccct
 360
 gggctctcag ggacccccctg ggtcggcttc tgtccctgtc acacccccaa cccagggag
 420
 gggctgtcat agtcccagag gataagcaat acctatttct gactgagtct cccagcccag
 480
 acccaggac cctggccccca agctcagctc taagaaccgc caccaacccc tccagctcca
 540
 aatctgagcc tccaccacat agactgaaac tccctggcc ccagccctct cctgcctggc
 600
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 658

<210> 12

<211> 1507

<212> DNA

<213> H. sapiens

<220>

<221> misc_feature

<222> 1047, 1301

<223> n = A,T,C or G

<400> 12

ggaacgcaga gcggagcgtg gagagcggag cgaagctgga taacagggga ccgatgatgt
 60
 ggcgaccatc agttctgctg cttctgttgc tactgaggca cggggcccag gggaagccat
 120
 cccagacgc aggcctcat ggccagggga ggtgacacca ggcgccccct ctgagcgacg
 180
 ctccccatga tgacgccac gggaacttcc agtacgacca tgaggcttct ctgggacggg
 240
 aagtggccaa ggaattcgac caactacccc cagaggaaaag ccaggcccgt ctggggcgga
 300
 tcgtggaccg catggaccgc gcgggggacg gcgacggctg ggtgtcgctg gccagcttc
 360

gcgcgtggat cgcgcacacg cagcagcggc acatacggga ctcggtgagc gcggcctggg
 420
 acacgtacga cacggaccgc gacgggcgtg tgggttggga ggagctgcgc aacgccacct
 480
 atggccacta cgcgcccggt gaagaatttc atgacgtgga ggatgcagag acctacaaaa
 540
 agatgctggc tcgggacgag cggcgtttcc ggggtggccga ccaggatggg gactcgatgg
 600
 ccactcgaga ggagctgaca gccttcctgc accccgagga gttccctcac atgcggggaca
 660
 tcgtgattgc tgaaaccctg gaggacctgg acagaaacaa agatggctat gtccagggtg
 720
 aggagtacat cgcggatctg tactcagccg agcctgggga ggaggagccg gcgtgggtgc
 780
 agacggagag gcagcagttc cgggacttcc gggatctgaa caaggatggg cacctggatg
 840
 ggagtgaggt gggccactgg gtgctgcccc ctgcccagga ccagcccctg gtggaagcca
 900
 accacctgct gcacgaragc gacacggaca aggaygggcg gctgagcaaa gcgsaaatcc
 960
 tgggtaattg gaacatgttt gtgggcagtc aggccaccaa ctatggygag gacctgacct
 1020
 ggcaccacga tgagctgtga gcmccngca cctgccacag cctcagaggc ccgcacaatg
 1080
 accggaggag gggccgctgt ggtctggccc cctccctgtc caggccccgc aggaggcaga
 1140
 tgcagtccca ggcatectcc tkccctggg ctctcagga cccctgggt cggcttctgt
 1200
 cctgtcaca cccccaacct caggaggagg ctgtcatagt cccagaggat aagcaatacc
 1260
 tattttctgac tgagtctccc agcccagacc caggggacct nggccccaaag ctgagctcta
 1320
 agaaccgccc caaccctcc agctccaaat ctgagcctcc accacataga ctgaaactcc
 1380
 cctggcccca gccctctcct gcctggcctg gcctgggaca cctcctctct gccaggaggc
 1440
 aataaaaagcc agcgcgcggga aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa
 1500
 aaaaaaan
 1507

<210> 13
 <211> 661
 <212> DNA
 <213> H. sapiens

<220>
 <221> CDS
 <222> (79) ... (376)

<400> 13
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 60
 tgacttgcag ggtccgcc atg gag cca gag cag atg ctg gag gga caa acg
 111

Met Glu Pro Glu Gln Met Leu Glu Gly Gln Thr
 1 5 10

cag gtt gca gaa aat cct cac tct gag tac ggt ctc aca gac aac gtt
159

Gln Val Ala Glu Asn Pro His Ser Glu Tyr Gly Leu Thr Asp Asn Val
15 20 25

gag aga ata gta gaa aat gag aag att aat gca gaa aag tca tca aag
207

Glu Arg Ile Val Glu Asn Glu Lys Ile Asn Ala Glu Lys Ser Ser Lys
30 35 40

cag aag gta gat ctc cag tct ttg cca act cgt gcc tac ctg gat cag
255

Gln Lys Val Asp Leu Gln Ser Leu Pro Thr Arg Ala Tyr Leu Asp Gln
45 50 55

aca gtt gtg cct atc tta tta cag gga ctt gct gtg ctt gca aag gaa
303

Thr Val Val Pro Ile Leu Leu Gln Gly Leu Ala Val Leu Ala Lys Glu
60 65 70 75

aga cca cca aat ccc att gaa ttt cta gca tct tat ctt tta aaa aac
351

Arg Pro Pro Asn Pro Ile Glu Phe Leu Ala Ser Tyr Leu Leu Lys Asn
80 85 90

aag gca cag ttt gaa gat cga aac t gacttaatgg gaagaacaga
396

Lys Ala Gln Phe Glu Asp Arg Asn
95

aaaatttagt tgctactgta gatttacatg attaagaggc agctttaatt gccatgatca
456

ttccctcttt ttggatgtat aagaaccttc cggacaacag aacctatttc tggaattgca
516

gaagataaca tatttccctt attttgattt aatcaccata aaccatacct atttaagtga
576

tgtattctgt gcaatttttt tctcagattg tctttaactt tgtttttaaa atgaccttca
636

aaataaaactg tcaaaacacc attat
661

<210> 14

<211> 99

<212> PRT

<213> H. sapiens

<400> 14

Met Glu Pro Glu Gln Met Leu Glu Gly Gln Thr Gln Val Ala Glu Asn
1 5 10 15
Pro His Ser Glu Tyr Gly Leu Thr Asp Asn Val Glu Arg Ile Val Glu
20 25 30
Asn Glu Lys Ile Asn Ala Glu Lys Ser Ser Lys Gln Lys Val Asp Leu
35 40 45
Gln Ser Leu Pro Thr Arg Ala Tyr Leu Asp Gln Thr Val Val Pro Ile
50 55 60
Leu Leu Gln Gly Leu Ala Val Leu Ala Lys Glu Arg Pro Pro Asn Pro

ccctgtcaca cccccaaccc cagggagggg ctgtcatagt cccagaggat aagcaatacc
 1260
 tattttctgac tgagtctccc agcccagacc cagggaccct nggcccgaag ctcagctcta
 1320
 agaaccgccc caaccctcc agctccaaat ctgagcctcc accacataga ctgaaactcc
 1380
 cctggcccca gccctctcct gcctggcctg gcctgggaca cctcctctct gccaggagggc
 1440
 aataaaagcc agcgccggga aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa
 1500
 aaaaaan
 1507

<210> 16
 <211> 716
 <212> DNA
 <213> H. sapiens

<220>
 <221> CDS
 <222> (16)...(538)

<400> 16
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 51

Met Ala Asp Val Leu Asp Leu His Glu Ala Gly Gly
 1 5 10

gaa gat ttc gcc atg gat gag gat ggg gac gag agc att cac aaa ctg
 99

Glu Asp Phe Ala Met Asp Glu Asp Gly Asp Glu Ser Ile His Lys Leu
 15 20 25

aaa gaa aaa gcg aag aaa cgg aag ggt cgc ggc ttt ggc tcc gaa gag
 147

Lys Glu Lys Ala Lys Lys Arg Lys Gly Arg Gly Phe Gly Ser Glu Glu
 30 35 40

ggg tcc cga gcg cgg atg cgt gag gat tat gac agc gtg gag cag gat
 195

Gly Ser Arg Ala Arg Met Arg Glu Asp Tyr Asp Ser Val Glu Gln Asp
 45 50 55 60

ggc gat gaa ccc gga cca caa cgc tct gtt gaa ggc tgg att ctc ttt
 243

Gly Asp Glu Pro Gly Pro Gln Arg Ser Val Glu Gly Trp Ile Leu Phe
 65 70 75

gta act gga gtc cat gag gaa gcc acc gaa gaa gac ata cac gac aaa
 291

Val Thr Gly Val His Glu Glu Ala Thr Glu Glu Asp Ile His Asp Lys
 80 85 90

ttc gca gaa tat ggg gaa att aaa aac att cat ctc aac ctc gac agg
 339

Phe Ala Glu Tyr Gly Glu Ile Lys Asn Ile His Leu Asn Leu Asp Arg
 95 100 105

cga aca gga tat ctg aag ggg tat act cta gtt gaa tat gaa aca tac
387

Arg Thr Gly Tyr Leu Lys Gly Tyr Thr Leu Val Glu Tyr Glu Thr Tyr
110 115 120

aag gaa gcc cag gct gct atg gag gga ctc aat ggc cag gat ttg atg
435

Lys Glu Ala Gln Ala Ala Met Glu Gly Leu Asn Gly Gln Asp Leu Met
125 130 135 140

gga cag ccc atc agc gtt gac tgg tgt ttt gtt cgg ggt cca cca aaa
483

Gly Gln Pro Ile Ser Val Asp Trp Cys Phe Val Arg Gly Pro Pro Lys
145 150 155

ggc aag agg aga ggt ggc cga aga cgc agc aga agt cca gac cgg aga
531

Gly Lys Arg Arg Gly Gly Arg Arg Arg Ser Arg Ser Pro Asp Arg Arg
160 165 170

cgt cgc t gacaggtcct ctgttggtcca ggtgttctct tcaagattcc atttgaccat
588

Arg Arg

gcagccttgg acaaatagga ctgggggtgga acttgctgtg tttatattta atctcttacc
648

gtatatgcgt agtatttgag ttgcgaataa atgttccatt ttgttttcta caaaaaaaaa
708

aaaaaaaa

716

<210> 17

<211> 174

<212> PRT

<213> H. sapiens

<400> 17

Met Ala Asp Val Leu Asp Leu His Glu Ala Gly Gly Glu Asp Phe Ala
1 5 10 15

Met Asp Glu Asp Gly Asp Glu Ser Ile His Lys Leu Lys Glu Lys Ala
20 25 30

Lys Lys Arg Lys Gly Arg Gly Phe Gly Ser Glu Glu Gly Ser Arg Ala
35 40 45

Arg Met Arg Glu Asp Tyr Asp Ser Val Glu Gln Asp Gly Asp Glu Pro
50 55 60

Gly Pro Gln Arg Ser Val Glu Gly Trp Ile Leu Phe Val Thr Gly Val
65 70 75 80

His Glu Glu Ala Thr Glu Glu Asp Ile His Asp Lys Phe Ala Glu Tyr
85 90 95

Gly Glu Ile Lys Asn Ile His Leu Asn Leu Asp Arg Arg Thr Gly Tyr
100 105 110

Leu Lys Gly Tyr Thr Leu Val Glu Tyr Glu Thr Tyr Lys Glu Ala Gln
115 120 125

Ala Ala Met Glu Gly Leu Asn Gly Gln Asp Leu Met Gly Gln Pro Ile
130 135 140

Ser Val Asp Trp Cys Phe Val Arg Gly Pro Pro Lys Gly Lys Arg Arg
 145 150 155 160
 Gly Gly Arg Arg Arg Ser Arg Ser Pro Asp Arg Arg Arg Arg
 165 170

<210> 18
 <211> 763
 <212> DNA
 <213> H. sapiens

<220>
 <221> CDS
 <222> (2)...(551)

<400> 18
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 49

Met Ala Lys Pro Cys Gly Val Arg Leu Ser Gly Glu Ala Arg Lys Gln
 1 5 10 15

gtg gag gtc ttc aga cag aat ctt ttc cag gag gct gag gaa ttc ctc
 97
 Val Glu Val Phe Arg Gln Asn Leu Phe Gln Glu Ala Glu Glu Phe Leu
 20 25 30

tac aga ttc ttg cca cag aaa atc ata tac ctg aat cag ctc ttg caa
 145
 Tyr Arg Phe Leu Pro Gln Lys Ile Ile Tyr Leu Asn Gln Leu Leu Gln
 35 40 45

gag gac tcc ctc aat gtg gct gac ttg act tcc ctc cgg gcc cca ctg
 193
 Glu Asp Ser Leu Asn Val Ala Asp Leu Thr Ser Leu Arg Ala Pro Leu
 50 55 60

gac atc ccc atc cca gac cct cca ccc aag gat gat gag atg gaa aca
 241
 Asp Ile Pro Ile Pro Asp Pro Pro Pro Lys Asp Asp Glu Met Glu Thr
 65 70 75 80

gat aag cag gag aag aaa gaa gtc cct aag tgt gga ttt ctc cct ggg
 289
 Asp Lys Gln Glu Lys Lys Glu Val Pro Lys Cys Gly Phe Leu Pro Gly
 85 90 95

aat gag aaa gtc ctg tcc ctg ctt gcc ctg gtt aag cca gaa gtc tgg
 337
 Asn Glu Lys Val Leu Ser Leu Leu Ala Leu Val Lys Pro Glu Val Trp
 100 105 110

act ctc aaa gag aaa tgc att ctg gtg att aca tgg atc caa cac ctg
 385
 Thr Leu Lys Glu Lys Cys Ile Leu Val Ile Thr Trp Ile Gln His Leu
 115 120 125

atc ccc aag att gaa gat gga aat gat ttt ggg gta gca atc cag gag
 433
 Ile Pro Lys Ile Glu Asp Gly Asn Asp Phe Gly Val Ala Ile Gln Glu

130 135 140
 aag gtg ctg gag agg gtg aat gcc gtc aag acc aaa gtg aag ctt tcc
 481
 Lys Val Leu Glu Arg Val Asn Ala Val Lys Thr Lys Val Lys Leu Ser
 145 150 155 160
 aga caa cca ttt cca agt act tct cag aac gtg ggg atg ctg tgg cca
 529
 Arg Gln Pro Phe Pro Ser Thr Ser Gln Asn Val Gly Met Leu Trp Pro
 165 170 175
 agg cct cca agg aga ctc atg t aatggattac cgggccttgg tgcattgagcg
 581
 Arg Pro Pro Arg Arg Leu Met
 180
 agatgaggca gcctatgggg agctcagggc catggtgctg gacctgaggg ccttctatgc
 641
 tgagctttat catatcatca gcagcaacct ggagaaaatt gtcaacccaa aggggtgaaga
 701
 aaagccatct atgtactgaa cccgggacta gaaggaaaat aaatgatcta tatgttgtgt
 761
 gg
 763
 <210> 19
 <211> 183
 <212> PRT
 <213> H. sapiens
 <400> 19
 Met Ala Lys Pro Cys Gly Val Arg Leu Ser Gly Glu Ala Arg Lys Gln
 1 5 10 15
 Val Glu Val Phe Arg Gln Asn Leu Phe Gln Glu Ala Glu Glu Phe Leu
 20 25 30
 Tyr Arg Phe Leu Pro Gln Lys Ile Tyr Leu Asn Gln Leu Leu Gln
 35 40 45
 Glu Asp Ser Leu Asn Val Ala Asp Leu Thr Ser Leu Arg Ala Pro Leu
 50 55 60
 Asp Ile Pro Ile Pro Asp Pro Pro Pro Lys Asp Asp Glu Met Glu Thr
 65 70 75 80
 Asp Lys Gln Glu Lys Lys Glu Val Pro Lys Cys Gly Phe Leu Pro Gly
 85 90 95
 Asn Glu Lys Val Leu Ser Leu Leu Ala Leu Val Lys Pro Glu Val Trp
 100 105 110
 Thr Leu Lys Glu Lys Cys Ile Leu Val Ile Thr Trp Ile Gln His Leu
 115 120 125
 Ile Pro Lys Ile Glu Asp Gly Asn Asp Phe Gly Val Ala Ile Gln Glu
 130 135 140
 Lys Val Leu Glu Arg Val Asn Ala Val Lys Thr Lys Val Lys Leu Ser
 145 150 155 160
 Arg Gln Pro Phe Pro Ser Thr Ser Gln Asn Val Gly Met Leu Trp Pro
 165 170 175
 Arg Pro Pro Arg Arg Leu Met
 180
 <210> 20

<211> 790
 <212> DNA
 <213> H. sapiens

<220>
 <221> CDS
 <222> (240)...(585)

<400> 20
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 actttttgtg aaattcagat cgcagtgtgt catttacaaa tcttttgtct ttctttctggt
 120
 catctacacc ttttgcacag ttcttgaaga caacgtcatc atcccacctt cttttaactt
 180
 tgaagttggc ctgaggctgg gatgggccag tgagattaag gagagggttt ccgctcaga
 239
 atg ttt tcc ata cga atc ctc tct tct tca gct ttt tgt tct tgt tcc
 287
 Met Phe Ser Ile Arg Ile Leu Ser Ser Ser Ala Phe Cys Ser Cys Ser
 1 5 10 15
 ttc ctg gcc tgc tct tca gct ctt tct ttt tta att ttt tcc agt tct
 335
 Phe Leu Ala Cys Ser Ser Ala Leu Ser Phe Leu Ile Phe Ser Ser Ser
 20 25 30
 gca aga aga gct gca gta tca tca tca tca ctt tct tct tca aaa tct
 383
 Ala Arg Arg Ala Ala Val Ser Ser Ser Ser Leu Ser Ser Ser Lys Ser
 35 40 45
 tca tct tcc tca tct gtt aga ggg tca tct gca tca agg ttg gcg gca
 431
 Ser Ser Ser Ser Ser Val Arg Gly Ser Ser Ala Ser Arg Leu Ala Ala
 50 55 60
 gga atc tgg tct aac cgt ggc ttt ttt gac act gaa gag gag gtt gta
 479
 Gly Ile Trp Ser Asn Arg Gly Phe Phe Asp Thr Glu Glu Glu Val Val
 65 70 75 80
 tgt tct cgg gtt gga cga tcc cta ttt ttc tct ctt gca gca gct ctc
 527
 Cys Ser Arg Val Gly Arg Ser Leu Phe Phe Ser Leu Ala Ala Ala Leu
 85 90 95
 tct ctt tct tcc aac tct ctc ctg aag tca cgg tta cga acc tct tca
 575
 Ser Leu Ser Ser Asn Ser Leu Leu Lys Ser Arg Leu Arg Thr Ser Ser
 100 105 110
 ggg gca tcc t gagtagtctg tctgtatttt atctttgtat gagagggtag
 625
 Gly Ala Ser
 115

gtctctgctt gaatactgct ttgaaagttg gctcaaatca ccttctcctt ttccccctcc
685
acctctggca ggttcaaagg ttggcctggc tgctgttgc atcttttatg actggccgag
745
gtccgatgca gcaggctccg aagatcatat agacgccatt accac
790

<210> 21
<211> 115
<212> PRT
<213> H. sapiens

<400> 21
Met Phe Ser Ile Arg Ile Leu Ser Ser Ser Ala Phe Cys Ser Cys Ser
1 5 10 15
Phe Leu Ala Cys Ser Ser Ala Leu Ser Phe Leu Ile Phe Ser Ser Ser
20 25 30
Ala Arg Arg Ala Ala Val Ser Ser Ser Leu Ser Ser Ser Lys Ser
35 40 45
Ser Ser Ser Ser Ser Val Arg Gly Ser Ser Ala Ser Arg Leu Ala Ala
50 55 60
Gly Ile Trp Ser Asn Arg Gly Phe Phe Asp Thr Glu Glu Glu Val Val
65 70 75 80
Cys Ser Arg Val Gly Arg Ser Leu Phe Phe Ser Leu Ala Ala Ala Leu
85 90 95
Ser Leu Ser Ser Asn Ser Leu Leu Lys Ser Arg Leu Arg Thr Ser Ser
100 105 110
Gly Ala Ser
115

<210> 22
<211> 1939
<212> DNA
<213> H. sapiens

<220>
<221> CDS
<222> (53)...(1700)

<400> 22
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58

Met Lys
1

agg cct aag tta aag aaa gca agt aaa cgc atg acc tgc cat aag cgg
106
Arg Pro Lys Leu Lys Lys Ala Ser Lys Arg Met Thr Cys His Lys Arg
5 10 15

tat aaa atc caa aaa aag gtt cga gaa cat cat cga aaa tta aga aag
154
Tyr Lys Ile Gln Lys Lys Val Arg Glu His His Arg Lys Leu Arg Lys
20 25 30

gag gct aaa aag cag ggt cac aag aag cct agg aaa gac cca gga gtt
202
Glu Ala Lys Lys Gln Gly His Lys Lys Pro Arg Lys Asp Pro Gly Val

35	40	45	50
cca aac agt gct ccc ttt aag gag gct ctt ctt agg gaa gct gag cta			
250			
Pro Asn Ser Ala	Pro Phe Lys Glu Ala	Leu Leu Arg Glu Ala	Glu Leu
	55	60	65
agg aaa cag agg ctt gaa gaa cta aaa cag cag cag aaa ctt gac agg			
298			
Arg Lys Gln Arg	Leu Glu Glu Leu Lys Gln Gln Gln Lys	Leu Asp Arg	
	70	75	80
cag aag gaa cta gaa aag aaa aga aaa ctt gaa act aat cct gat att			
346			
Gln Lys Glu Leu Glu Lys Lys Arg Lys Leu Glu Thr Asn Pro Asp Ile			
	85	90	95
aag cca tca aat gtg gaa cct atg gaa aag gag ttt ggg ctt tgc aaa			
394			
Lys Pro Ser Asn Val Glu Pro Met Glu Lys Glu Phe Gly Leu Cys Lys			
	100	105	110
act gag aac aaa gcc aag tcg ggc aaa cag aat tca aag aag ctg tac			
442			
Thr Glu Asn Lys Ala Lys Ser Gly Lys Gln Asn Ser Lys Lys Leu Tyr			
	115	120	125
tgc caa gaa ctt aaa aag gtg att gaa gcc tcc gat gtt gtc cta gag			
490			
Cys Gln Glu Leu Lys Lys Val Ile Glu Ala Ser Asp Val Val Leu Glu			
	135	140	145
gtg ttg gat gcc aga gat cct ctt ggt tgc aga tgt cct cag gta gaa			
538			
Val Leu Asp Ala Arg Asp Pro Leu Gly Cys Arg Cys Pro Gln Val Glu			
	150	155	160
gag gcc att gtc cag agt gga cag aaa aag ctg gta ctt ata tta aat			
586			
Glu Ala Ile Val Gln Ser Gly Gln Lys Lys Leu Val Leu Ile Leu Asn			
	165	170	175
aaa tca gat ctg gta cca aag gag aat ttg gag agc tgg cta aat tat			
634			
Lys Ser Asp Leu Val Pro Lys Glu Asn Leu Glu Ser Trp Leu Asn Tyr			
	180	185	190
ttg aag aaa gaa ttg cca aca gtg gtg ttc aga gcc tca aca aaa cca			
682			
Leu Lys Lys Glu Leu Pro Thr Val Val Phe Arg Ala Ser Thr Lys Pro			
	195	200	205
aag gat aaa ggg aag ata acc aag cgt gtg aag gca aag aag aat gct			
730			
Lys Asp Lys Gly Lys Ile Thr Lys Arg Val Lys Ala Lys Lys Asn Ala			
	215	220	225

gct cca ttc aga agt gaa gtc tgc ttt ggg aaa gag ggc ctt tgg aaa
778

Ala Pro Phe Arg Ser Glu Val Cys Phe Gly Lys Glu Gly Leu Trp Lys
230 235 240

ctt ctt gga ggt ttt cag gaa act tgc agc aaa gcc att cgg gtt gga
826

Leu Leu Gly Gly Phe Gln Glu Thr Cys Ser Lys Ala Ile Arg Val Gly
245 250 255

gta att ggt ttc cca aat gtg ggg aaa agc agc att atc aat agc tta
874

Val Ile Gly Phe Pro Asn Val Gly Lys Ser Ser Ile Ile Asn Ser Leu
260 265 270

aaa caa gaa cag atg tgt aat gtt ggt gta tcc atg ggg ctt aca agg
922

Lys Gln Glu Gln Met Cys Asn Val Gly Val Ser Met Gly Leu Thr Arg
275 280 285 290

agc atg caa gtt gtc ccc ttg gac aaa cag atc aca atc ata gat agt
970

Ser Met Gln Val Val Pro Leu Asp Lys Gln Ile Thr Ile Ile Asp Ser
295 300 305

ccg agc ttc atc gta tct cca ctt aat tcc tcc tct gcg ctt gct ctg
1018

Pro Ser Phe Ile Val Ser Pro Leu Asn Ser Ser Ser Ala Leu Ala Leu
310 315 320

cga agt cca gca agt att gaa gta gta aaa ccg atg gag gct gcc agt
1066

Arg Ser Pro Ala Ser Ile Glu Val Val Lys Pro Met Glu Ala Ala Ser
325 330 335

gcc atc ctt tcc cag gct gat gct cga cag gta gta ctg aaa tat act
1114

Ala Ile Leu Ser Gln Ala Asp Ala Arg Gln Val Val Leu Lys Tyr Thr
340 345 350

gtc cca ggc tac agg aat tct ctg gaa ttt ttt act atg ctt gct cag
1162

Val Pro Gly Tyr Arg Asn Ser Leu Glu Phe Phe Thr Met Leu Ala Gln
355 360 365 370

aga aga ggt atg cac caa aaa ggt gga atc cca aat gtt gaa ggt gct
1210

Arg Arg Gly Met His Gln Lys Gly Gly Ile Pro Asn Val Glu Gly Ala
375 380 385

gcc aaa ctg ctg tgg tct gag tgg aca ggt gcc tca tta gct tac tat
1258

Ala Lys Leu Leu Trp Ser Glu Trp Thr Gly Ala Ser Leu Ala Tyr Tyr
390 395 400

tgc cat ccc cct aca tct tgg act cct cct cca tat ttt aat gag agt
1306

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Met	Lys	Arg	Pro	Lys	Leu	Lys	Lys	Ala	Ser	Lys	Arg	Met	Thr	Cys	His
1				5					10					15	
Lys	Arg	Tyr	Lys	Ile	Gln	Lys	Lys	Val	Arg	Glu	His	His	Arg	Lys	Leu
			20					25					30		
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Ala	Leu	Arg	Ser	Pro	Ala	Ser	Ile	Glu	Val	Val	Lys	Pro	Met	Glu	Ala
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 Glu Glu Lys Asp Ile His Glu Glu Leu Pro Lys Arg Lys Glu Arg Lys
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 Ile Val Leu Leu Arg Ala Leu Pro Val Pro Arg Ala Lys His Val Lys
 65 70 75

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 His Glu Leu Ala Glu Ile Val Phe Lys Val Gly Lys Val Ile Asp Pro

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Lys Leu Thr Thr Ala Ser Asn Phe Trp Ala Gln Val Ile Leu Ser Leu
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497
Pro Val Val Phe Val Asp Cys Leu Met Glu Ser His Gly Thr Arg Arg

45

50

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